

Genetics and Molecular Tools: USGS History in the Clinton Administration

Recent technological advances in molecular biology have revolutionized our basic understanding of biological and evolutionary processes. These contemporary applications have significantly enhanced USGS's ability to delineate the finest level of biological diversity -- that is, genetic diversity -- and have provided remarkably sensitive techniques for diagnosing the presence and effects of environmental degradation on a host of endangered, threatened, and at-risk species. No other federal agency has the staff, skills, or mandate to initiate genetic monitoring of critical biological resources at the national level. In the last 8 years, USGS has used DNA markers to identify "Distinct Population Segments" and "Evolutionarily Significant Units" (as defined in the Endangered Species Act) in spotted owls, piping plovers, Micronesian kingfishers, Snake River steelhead, Atlantic salmon, Atlantic sturgeon, lake trout, brook trout, horseshoe crabs, torrent salamanders, spotted salamanders, wood frogs, bog turtles, and other species. USGS, along with its international collaborators, has effectively used genetic characteristics to identify unique threatened fish populations in the Pacific Northwest, the Southwest, the Great Lakes, and the Eastern seaboard. Genetic and molecular tools have proved essential to USGS research on management strategies to restore, preserve, and maintain "natural" or "native" levels of genetic diversity in populations of Pacific salmon, Atlantic salmon, and lake trout. For example, USGS developed a molecular genetic technique that identifies the continent of origin (North America or Europe) of Atlantic salmon collected in the mixed-fishery off west Greenland. Managers can now accurately assess the impact this fishery is having on salmon returns in both continents. Genetics and molecular tools have been used effectively by USGS scientists in identifying the breeding origin of migratory waterbirds and shorebirds during the winter; this kind of monitoring has provided substantially greater detail and depth than traditional marking and banding methods. In the Arctic, USGS has used molecular markers to assess the population structures of secretive Arctic mammals and birds. Similarly, USGS recently completed a study monitoring grizzly bears in the Glacier National Park region by using DNA analyses of bear hair caught in "hair traps" in the study area. Likewise, this DNA technology has been used in mark and recapture studies in black bears, giving regional land managers the best bear population information that they've ever had. USGS is also using genetic and molecular tools to maintain health and control disease in at-risk species propagated in captivity, including Pacific salmon, Atlantic salmon, and lake trout, as well as in wild populations of at-risk species such as native Hawaiian birds. In fact, ongoing USGS molecular biology research on avian malaria and other diseases in endangered Hawaiian birds is providing one of the last glimmers of hope for these imperiled species. USGS has successfully used genetic tools to "screen" for the effects of contaminants in wildlife, including lesser scaup and white-faced ibis. Similarly, USGS has used molecular techniques to address such wildlife-disease problems as duck plague virus and the organisms that cause avian cholera and botulism. Genetics and molecular tools are critical to our understanding the introduction of invasive species; such tools are allowing USGS to assess bio-control methods for parasitic sea lampreys in the Great Lakes.

